

**SEARCH REQUEST FORM**

Scientific and Technical Information Center

Requester's Full Name: \_\_\_\_\_ Examiner #: \_\_\_\_\_ Date: \_\_\_\_\_  
 Art Unit: \_\_\_\_\_ Phone Number 30 \_\_\_\_\_ Serial Number: \_\_\_\_\_  
 Mail Box and Bldg/Room Location: \_\_\_\_\_ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

\*\*\*\*\*

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: \_\_\_\_\_

Inventors (please provide full names): \_\_\_\_\_

Earliest Priority Filing Date: \_\_\_\_\_

*\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

**STAFF USE ONLY****Type of Search****Vendors and cost where applicable**

Searcher <u>factb</u>	NA Sequence (#) _____	STN _____
Searcher Phone # _____	AA Sequence (#) _____	Dialog _____
Searcher Location _____	Structure (#) _____	Quest/Other _____
Date Searcher Picked Up _____	Bibliographic _____	Dr Link _____
Date Completed <u>9-19-01</u>	Litigation _____	Lexis Nexis _____
Searcher Prep & Review Time _____	Fulltext _____	Sequence Systems _____
Clencal Prep Time _____	Patent Family _____	WWW/Internet _____
Online Time _____	Other _____	Other (specify) _____

us-09-285-480-175.rst

Express Mail No. EV207710889US

530 ttgtttcaaaagaaatgaattttatgtgagtaataatataataaagagtggt 589  
 432 ttgtttcaaaagaaatgaattttatgtgagtaataatataataaagagtggt 491  
 590 ccatcaaccattctgaagctcaaggaataccaaagcctaaataatcaatca 649  
 492 ccatcaaccattctgaagctcaaggaataccaaagcctaaataatcaatca 551  
 650 tgcggagatgctc 663  
 552 tgcaggagatgctc 565

RESULT 2  
 A1687645/c 694 bp mRNA EST 27-MAY-1999  
 LOCUS A1687645.1 NC1-CCAP-U3 Homo sapiens cDNA clone IMAGE:2205805 3'  
 DEFINITION Similar to TR:060311 060311 KIAA0565 PROTEIN. ; mRNA sequence.

ACCESSION A1687645  
 VERSION A1687645.1 GI:4898939  
 KEYWORDS EST.  
 SOURCE human.

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 694)  
 NC1-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP).  
 Tumor Gene Index  
 Unpublished (1997)  
 On Apr 7, 1998 this sequence version replaced gi:3035554.  
 Contact: Robert Strausberg, Ph.D.  
 Tel: (301) 496-1550  
 Email: Robert.Strausberg@nih.gov  
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
 Emmert-Buck, M.D., Ph.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA Sequencing by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NC1-CCAP clone distribution information can be  
 found through the I-M.A.G.E. Consortium/LLNL at:  
[www.bio.lnl.gov/bbrp/image/image.html](http://www.bio.lnl.gov/bbrp/image/image.html)  
 Seq primer: -400P from Gibco  
 High quality sequence stop: 405.

FEATURES  
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 /tissue\_type="poorly-differentiated endometrial  
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 /notes="Organ: uterus; Vector: pCMV-SPORT6; Site:1; Salt:  
 Site:2; Not: Cloned unidirectionally. Primer: Oligo dt.  
 Average insert size 1.45 kb. Life technologies catalog #:  
 11541-018"

BASE COUNT 152 a 148 c 121 g 269 t 4 others  
 ORIGIN

Query Match 18.9% Score 228; DB 43; Length 694;  
 Best Local Similarity 62.1%; Pred. No. 1e-39;  
 Matches 427; Conservative 0; Mismatches 249; Indels 12; Gaps 4;

Qy 349 aagttctgagctgagaaacacatgctcacttcaatt--gaagaaacacagaca 405  
 Db 693 AACATCTGGCAGCTGAGACAAATTAATCAATTTCTGAAGTGGAGATGGGNACAGACCC 634  
 Qy 406 aagaaatactagagcagaattgaatacacacacatcctagactgctctgtgatacaag 465  
 Db 633 AGAAAGAGACTAGANNATAGAAATGNATCATACCGTGGTAGACTGGCTGCTGCTGACGTG 574

Qy 466 accatgacaaattgtgacatcaagaaagtcgaagcctgtttccacattgcaggag 525  
 Db 573 ACTGTGATCAAAAGTACAGACGCAAGAGA...CCTAAAGCTTGAATTCAGAGACAAGACA 517  
 Qy 526 a-----tgcttttgcgaagaaatgaattgtgtgagtagtacgatatataacaa 580  
 Db 516 AGAGTGGGTTCGTTTACATGACANAATGAAGTTTGTATGTCTGGCCTACAGCTAAGAA 457  
 Qy 581 tgaggtgctccatcaaccactttctgaagctcaaggaataccaaagcctaaataatca 640  
 Db 456 TGAGATTCTTCTGAAAGAACTTTCTTAATGCTGAAGTAAATTAACAGCCTACAAATTC 397  
 Qy 641 tctcaattatgcggagatgctcttaagagaaaaatacattgtgttccagacatgcacaaag 700  
 Db 396 GTCCATACACAAGAGATGCTCTTGAAGAGAGAGTTTGAATTTGGAACGTGTGCAAG 337  
 Qy 701 agaccaacgtgaacacacagctgctcaaatgaaggaagcgtgaacacacatgtatcaacaa 760  
 Db 336 AGACCTCAGCAACACAGCTGTGAGAAAGAAAGAACTGAACAAATGTACCAAAATGGAACA 277  
 Qy 761 agataatgtgaacaaacacaca-ctgaacagcaggagctctctgagaggaataattattcc 819  
 Db 276 AAGCAAACTGAAGAAATACATTTGCCAAGCAGGAATCTGTAGAGAGAGATTATCTCAAC 217  
 Qy 820 tacaagcaaaatattgtgcttcaacagcaattatgctgacacacacatgaagaaagctgaca 879  
 Db 216 TACTAAGTGAATATACGTTGCTTCACAGCAACTGGATGATGCTCACAAGAAAGCTAACA 157  
 Qy 880 acaaaagcaagatacaaatgtatcttcttctgagaggaataattgaacatcatctcc 939  
 Db 156 GTCAGAAAGAACAGACAGAGTACTATCCAGACCACTTTTCATTCCTGCTGCAAAATCTTC 97  
 Qy 940 taaaaggaagaaatgagagagatatttataataaccatttataaaacacgttatatac 999  
 Db 96 AAGCTGAGAGTGAAGAAAGCAGATTTCTTCACTACAAGAGAAAGAACAGAGAGCTGTGATG 37  
 Qy 1000 aatatgaagaaagagaaagcagaaacaga 1027  
 Db 36 AATATAATCATTTAAAGAAAGAAATGGA 9

RESULT 3  
 AFI09301 1068 bp mRNA EST 28-JAN-2000  
 LOCUS AFI09301 Homo sapiens prostate adult Homo sapiens cDNA clone  
 DEFINITION IPCA-6, mRNA sequence.

ACCESSION AFI09301  
 VERSION AFI09301.1 GI:6782694  
 KEYWORDS EST.  
 SOURCE human.

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 1068)  
 Walker,M.G., Volkmut,W., Sprinzak,E., Hodgson,D. and Klingler,T.  
 Prediction of gene function by genome-scale expression analysis:  
 prostate cancer-associated genes  
 Genome Res. 9 (12), 1198-1203 (1999)

JOURNAL 20082966  
 MEDLINE  
 COMMENT On Dec 5, 1997 this sequence version replaced gi:2662724.  
 Contact: Walker MG  
 Incyte Pharmaceuticals  
 3174 Porter Drive, Palo Alto, CA 94304, USA  
 co-expressed with known prostate-cancer genes.

FEATURES  
 source  
 1..1068  
 /organism="Homo sapiens"  
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 /clone\_lib="IPCA-6"  
 /tissue\_type="Homo sapiens prostate adult"  
 /dev\_stage="adult"  
 /note="Multiple clone assembly from multiple libraries and



us-09-285-480-175.rng

Sat Aug 26 19:26:24 2000

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 24, 2000, 20:27:28 : Search time 64.49 Seconds

(without alignments)  
4678.736 Million cell updates/sec

Title: US-09-285-480-175

Perfect score: 1206

Sequence: 1 ggcacgaggaagttttgtgt.....cgggtggtgctgctgtgcc 1206

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 311585 seqs, 145096042 residues

Total number of hits satisfying chosen parameters: 623170

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: N\_Geneseq\_36.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	149.4	12.4	367	V90219	EST clone DF670. N
2	69.4	5.8	1216	T66409	DNA encoding haema
3	68.4	5.7	664	X33181	Base sequence of t
4	68.4	5.7	7372	X33182	Base sequence of t
5	68.4	5.7	7797	X33180	Cowpox virus bsr f
6	68.4	5.7	7996	X33184	Base sequence of t
7	63.8	5.3	9789	T41852	cDNA encoding Plas
8	59.4	4.9	3399	T05868	Chicken leucocytot
9	56.4	4.7	110000	X20348_03	Continuation (4 of
10	54.6	4.5	1686	Q87387	DNA encoding Leuco
11	54.2	4.5	19124	T72882	Plasmodium var-7 g
12	53.8	4.5	5181	O80911	Plasmodium falcipa
13	52.6	4.4	4237	V61487	Human secreted pro
14	52.6	4.4	116624	V52850	Human eval gene co
15	50.2	4.2	4663	X20373	Borrelia burgdorfe
16	49.8	4.1	110000	X20348_02	Continuation (3 of
17	48.2	4.0	2487	X20398	Borrelia burgdorfe
18	46.8	3.9	2892	X20392	Borrelia burgdorfe
19	45.2	3.7	4673	Q27189	P. yoelii SSP2 ant
20	44.8	3.7	1269	X20328	Borrelia burgdorfe
21	44.6	3.7	4590	N60472	Sequence encoding
22	44.6	3.7	110000	V21209_13	Continuation (14 o
23	44.4	3.7	4766	Q70102	Malarial PfEMP3 ep
24	44	3.6	1671	Q24134	50 kD subunit of S
25	44	3.6	9399	X20361	Borrelia burgdorfe
26	43.8	3.6	110000	V21209_02	Continuation (3 of
27	43.2	3.6	240	T76782	Staphylococcus aur
28	43.2	3.6	3095	Q03875	Sequence encoding
29	42.8	3.5	2447	V54387	Human secretory pr
30	42.4	3.5	110000	X20348_08	Continuation (9 of
31	42	3.5	2973	Q53501	Sequence of bean m
32	42	3.5	35515	X20352	Borrelia burgdorfe
33	41.8	3.5	1956	T67161	Plasmodium falcipa

Human pro-urokinas  
B. burgdorferi Osp  
Streptococcus pneu  
Continuation (7 of  
Continuation (7 of  
NF-YB. Expression  
Mannose-1-phosphat  
P. falciparum gp19  
Sequence encoding  
Human secreted pro  
Nucleotide sequenc  
DNA encoding an an

34 41.6 3.4 2427 1 Q04107  
35 41.4 3.4 1498 1 Q83837  
36 41.2 3.4 1453 1 T61724  
37 41.2 3.4 110000 1 V21209\_06  
38 40.8 3.4 110000 1 X20248\_06  
39 40.6 3.4 1284 1 Q15361  
40 40.6 3.4 4000 1 T51902  
41 40.6 3.4 4940 1 V35363  
42 40.6 3.4 5760 1 N50530  
43 40.4 3.3 819 1 X04370  
44 40.2 3.3 202 1 V41451  
45 40.2 3.3 1434 1 X16007

## ALIGNMENTS

## RESULT 1

V90219

NC V90219

DT 15-FEB-1999 (first entry)

DE EST clone DF670.

KW Human; secreted protein; expressed sequence tag; EST; haematopoiesis;

KW tissue growth; activin; inhibitor; chemotaxis; chemokinesis; haemostatic;

KW receptor; ligand; thrombolytic; anti-inflammatory; cadherin; anti-tumour;

KW gene therapy; ss.

OS Homo sapiens.

PN W09845436-A2.

PD 15-OCT-1998.

PF 10-APR-1998: U06955.

PR 10-APR-1997: US-938821.

PA (GENY) GENETICS INST INC.

PI Agostino M, Jacobs K, Lavallie ER, McCoy JM, Merberg D.

PI Racie LA, Spaulding V, Treacy M;

DR WPI: 99-070077/06.

PT New polynucleotides encoding human secreted proteins - derived from

PT e.g. human blood, kidney, foetal lung, placenta, testes, brain,

PT ovary, pituitary, retina and colon cDNA libraries.

PS Claim 1; Page 469; 618pp; English.

CC The present sequence represents a human expressed sequence tag (EST).

CC The polynucleotide, which is a secreted EST, and the encoded protein

CC are predicted to have useful biological activities which would make

CC them suitable for treating, preventing or ameliorating medical

CC conditions in humans and animals, although no supporting data is

CC given. Suggested activities include nutritional activity, immune

CC stimulating or suppressing activity, haematopoiesis regulating

CC activity, tissue growth activity, activin/inhibin activity,

CC chemotactic/chemokinetic activity, haemostatic and thrombolytic

CC activity, receptor/ligand activity, anti-inflammatory activity,

CC cadherin/tumour invasion suppressor activity, tumour inhibition

CC activity. The polynucleotide may also be useful for gene therapy.

CC Sequence 367 BP; 158 A; 53 C; 79 G; 77 T;

Query Match 12.4%; Score 149.4; DB 1; Length 367;

Best Local Similarity 67.5%; Pred. No. 4.1e-24;

Matches 241; Conservative 0; Mismatches 86; Indels 30; Gaps

QY 683 ttcagacatgcacaaagagacacacagctgaaacacagctgcaaatgaaggagctgaaca 742

DB 4 TTTAAGCGGGTACAAAGGACCTTAAGCCAAACACAGCTGTCAAATGAAGGAATGAACA 63

QY 743 catgtatcaaaacgaacaaagataatgtgaaacacacactgaacagcagggagctcttaga 802

DB 64 AAAGTATCAAAATGACAAAGTAAAGTGATTAATATACATTGGAAGCAGGAGTCTGTAGA 123

QY 803 tcagaaattatttcaactacaaagacaaataatgtgcttcaacagcaaatagttctatgc 862

DB 124 GGAGAGATTGCTCTCACTACAAAGTGAGATATGTTGCTGCACAAACAACTGGATGTC 183

QY 863 acataagaaagctgacacacaaagataacaaattgattatca..... 907

